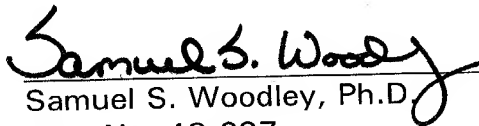


REMARKS

Claims 1-27 are pending in this application. The specification and claims have been amended solely to introduce the appropriate sequence identifiers (*i.e.*, the SEQ ID NOS) in the accompanying Sequence Listing. Thus, no new matter has been introduced and Claims 1-27 will remain pending upon entry of these amendments. Entry of these amendments is therefore respectfully requested.

Respectfully submitted,

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EXHIBIT A

EXHIBIT A:
SPECIFICATION AND CLAIM AMENDMENTS TO
U.S. PATENT APPLICATION SERIAL NO. 09/910,943
(ATTORNEY DOCKET NO. 7529/1G148US1)

SUBMITTED PURSUANT TO 37 C.F.R. § 1.121

IN THE SPECIFICATION:

The specification should be amended as follows:

The paragraph at lines 1-8 on page 3 of the specification should be amended as follows:

-- The present invention provides a nucleic acid array containing a single nucleic acid species of a *Xenopus* embryonic gene product set forth in Appendix 1 (SEQ ID NOS: 2-742). In addition, the invention provides an isolated nucleic acid comprising a sequence corresponding to or complementary to a sequence of not less than 20, preferably not less than 50, and more preferably not less than 100, contiguous nucleotides of any one of the sequences of Appendix 1 (SEQ ID NOS: 2-742). These sequences correspond to the gene products listed in the tables of Appendix 2, as can readily be determined by one of ordinary skill from the sequence information. --

The paragraph at lines 1-8 on page 14 of the specification should be amended as follows:

-- The terms "mutant" and "mutation" mean any detectable change in genetic material, *e.g.* DNA, or any process, mechanism, or result of such a change. This includes gene mutations, in which the structure (*e.g.* DNA sequence) of a gene is altered, any gene or DNA arising from any mutation process, and any expression product (*e.g.* protein or enzyme) expressed by a modified gene or DNA sequence. The term "variant" may also be used to indicate a modified or altered gene, DNA sequence, enzyme, cell, etc., *i.e.*, any kind of mutant. The present invention includes mutants and variants of the [sequence] sequences of Appendix 1 (SEQ ID NOS:2-742), which are the gene products listed in Appendix 2. --

The paragraph at lines 9-13 on page 14 of the specification as filed should be amended as follows:

-- "Sequence-conservative variants" of a polynucleotide sequence are those in which a change of one or more nucleotides in a given codon position results in no alteration in the amino acid encoded at that position. The invention includes sequence-conservative variants of the sequences of Appendix 1 (SEQ ID NOS:2-742), which are the gene products listed in Appendix 2. --

The paragraph starting on page 14, line 14 and ending on page 15, line 5 of the specification as filed should be amended as follows:

-- "Function-conservative variants" are those in which a given amino acid residue in a protein or enzyme has been changed without altering the overall conformation and function of the polypeptide, including, but not limited to, replacement of an amino acid with one having similar properties (such as, for example, polarity, hydrogen bonding potential, acidic, basic, hydrophobic, aromatic, and the like). Amino acids with similar properties are well known in the art. For example, arginine, histidine and lysine are hydrophilic-basic amino acids and may be interchangeable. Similarly, isoleucine, a hydrophobic amino acid, may be replaced with leucine, methionine or valine. Such changes are expected to have little or no effect on the apparent molecular weight or isoelectric point of the protein or polypeptide. Amino acids other than those indicated as conserved may differ in a protein or enzyme so that the percent protein or amino acid sequence similarity between any two proteins of similar function may vary and may be, for example, from 70% to 99% as determined according to an alignment scheme such as by the Cluster Method, wherein similarity is based on the MEGALIGN algorithm. A "function-conservative variant" also includes a polypeptide or enzyme which has at least 60 % amino acid identity as determined by BLAST or FASTA algorithms, preferably at least 75%, most preferably at least 85%, and even more preferably at least 90%, and which has the same or substantially similar properties or functions as the native or parent protein or enzyme to which it is compared. The invention

includes sequence-conservative variants of the sequences of Appendix 1 (SEQ ID NOS:2-742), which are the gene products listed in Appendix 2. --

The paragraph at lines 6-15 on page 15 of the specification as filed should be amended as follows:

-- As used herein, the term "homologous" in all its grammatical forms and spelling variations refers to the relationship between proteins that possess a "common evolutionary origin," including proteins from superfamilies (*e.g.*, the immunoglobulin superfamily) and homologous proteins from different species (*e.g.*, myosin light chain, etc.) (Reeck *et al.*, Cell 50:667, 1987). Such proteins (and their encoding genes) have sequence homology, as reflected by their sequence similarity, whether in terms of percent similarity or the presence of specific residues or motifs at conserved positions. The invention includes one or more homologous coding sequences to those set forth in Appendix 1 (SEQ ID NOS:2-742), which are the gene products listed in Appendix 2, particularly homologs from other species (orthologs), such as humans. --

The paragraph beginning at page 33, line 26 and ending at page 34, line 10 of the specification as filed should be amended as follows:

-- The 768 different clones were then sequenced from the 5'-end on ABI 3700 sequencers using Big Dye chemistry with a sequencing primer,

designated SP6-22 (SEQ ID NO:1), having the nucleotide sequence: 5'-CTTGATTTAGGTGACACTATAG-3' (SP6-22; SEQ ID NO:1). The sequences were analyzed and organized using the automated sequence annotation tool MAGPIE (Gaasterland and Sensen, Trends Genet.1996, 12:76; Gaasterland and Sensen, Biochimie 1996, 78:302). The Xenopus sequences from each of the sequenced clones are provided in Appendix 1 (SEQ ID NOS:2-742). These clones were organized into eight blocks (S10-1 through S10-8) of 96 clones corresponding to the 96 well block in which the clones were incubated. The Table in Appendix 2 from MAGPIE summarizes all the information gathered together for the 768 clones and includes a specific identification number, the size in base-pairs and the description for each gene. The Table shows that a number of the novel genes were identified from the clones and may play an important role in the process of embryogenesis. --

IN THE CLAIMS:

Claims 1, 6-8 and 23 should be amended as follows:

1. (Once amended) A nucleic acid array, wherein each coordinate of the array contains a single nucleic acid species, which nucleic acid species has a sequence of a Xenopus embryonic gene product set forth in Appendix 1 (SEQ ID

NOS:2-742), or the complement thereof, or a hybridizable fragment thereof consisting of not less than 20 contiguous nucleotides from the sequence.

6. (Once amended) An isolated nucleic acid comprising a sequence corresponding to or complementary to a sequence of not less than 20 contiguous nucleotides of any one of the sequences of Appendix 1 (SEQ ID NOS:2-742).

7. (Once amended) The nucleic acid of claim 6 wherein the sequence consists of [the] a sequence of Appendix 1 (SEQ ID NOS:2-742), or [the] a complement thereof.

8. (Once amended) The nucleic acid of claim 6 wherein the sequence lacks any homology to a known sequence as set forth in the list in Appendix 1 (SEQ ID NOS:2-742).

23. (Once amended) The method according to claim 9, wherein the nucleic acid array contains one or more sequences from Appendix 1 (SEQ ID NOS:2-742).